

Rec'd PCT/PTO 13 APR 2005

**10/530393**

**RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/530,393

Source: PG/10

Date Processed by STIC: 4/13/05

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PCT

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/530,393**

**DATE: 04/13/2005**  
**TIME: 09:42:26**

**Input Set : D:\8449304999.txt**  
**Output Set: N:\CRF4\04132005\J530393.raw**

3 <110> APPLICANT: LeClair, Ken  
 4 Srivastava, Pramod K.  
 6 <120> TITLE OF INVENTION: Heat Shock Protein Binding Fragments of CD91, and Uses  
 Thereof  
 8 <130> FILE REFERENCE: 8449-304-999  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/530,393  
 C--> 10 <141> CURRENT FILING DATE: 2005-04-04  
 10 <150> PRIOR APPLICATION NUMBER: PCT/US03/32167  
 11 <151> PRIOR FILING DATE: 2003-10-07  
 13 <150> PRIOR APPLICATION NUMBER: 60/416,821  
 14 <151> PRIOR FILING DATE: 2002-10-07  
 16 <160> NUMBER OF SEQ ID NOS: 17  
 18 <170> SOFTWARE: PatentIn version 3.2  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 2553  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: H. sapiens  
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 28 atcgacgccc ctaagacttg cagccccaaag cagttgcct gcagagatca aataacctgt 120  
 30 atctcaaagg gctggcggtg cgacggtagag agggactgcc cagacggatc tgacgaggcc 180  
 32 cctgagattt gtccacagag taaggccccag cgatgccagc caaacgagca taactgcctg 240  
 34 ggtactgagc tgggtgttcc catgtcccgcc ctctgcaatg gggtccagga ctgcatggac 300  
 36 ggctcagatg agggggccca ctgcccggagag ctccaaggca actgctctcg cctgggctgc 360  
 38 cagcaccatt gtgtccccac actcgatggg cccacactgct actgcaacag cagctttcag 420  
 40 cttcaggccag atggcaagac ctgcaaaagat tttgtatgagt gtcagtgtt cggcacctgc 480  
 42 agccagctat gcaccaaacac agacggctcc ttcatatgtg gtcgtgttga aggataacctc 540  
 44 ctgcagccgg ataaccgctc ctgcaaggcc aagaacgagc cagtagaccg gccccctgtg 600  
 46 ctgttgcatacc ccaactccca gaacatcttgc gcccacgttacc tgagtggggc ccagggtgtct 660  
 48 accatcacac ctacgagcac gcggcagacc acagccatgg acttcagcta tgccaaacgag 720  
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 54 cacgtggAAC agatggccat cgactggctg acaggcaact tctactttgt ggatgacatc 900  
 56 gatgatagga tctttgtctg caacagaaaat ggggacacat gtgtcacatt gctagacctg 960  
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82	ccccgagccc tggacttcca cgctgagacc ggcttcatct actttgccga caccaccagc	1740
84	tacctcattg gccgcccagaa gattgatggc actgagcggg agaccatcct gaaggacggc	1800
86	atccacaatg tggagggtgt ggccgtggac tggatggag acaatctgta ctggacggac	1860
88	gatggggcca aaaagacaat cagcgtggcc aggctggaga aagctgctca gaccgcgaag	1920
90	actttaatcg agggcaaaaat gacacacccc agggcttattg tggtgatcc actcaatggg	1980
92	tggatgtact ggacagactg ggaggaggac cccaaggaca gtcggcgtgg gcggctggag	2040
94	agggcgtgga tggatggctc acaccgagac atcttgcata cctccaagac agtgcgttgg	2100
96	cccaatgggc taagcctgga catcccgct gggccctct actgggtgga tgccttctac	2160
98	gaccgcatacg agacgatact gctcaatggc acagaccggaa agattgtgta tgaaggccct	2220
100	gagctgaacc acgccttgg cctgtgtcac catggcaact acctttctg gactgagttat	2280
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104	cttctgcgca gtgagcggcc cccatctt gagatccgaa tgtatgtgc ccagcagcag	2400
106	caagttggca ccaacaaatg ccgggtgaaac aatggcggct gcagcagcct gtgcttggcc	2460
108	acccttggga gccgcctgtg cgcctgtgt gaggaccagg tggaccagg tggaccgcgca agacggcgta	2520
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116	<213> ORGANISM: H. sapiens	
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125	20 25 30	
128	Ala Cys Arg Asp Gln Ile Thr Cys Ile Ser Lys Gly Trp Arg Cys Asp	
129	35 40 45	
132	Gly Glu Arg Asp Cys Pro Asp Gly Ser Asp Glu Ala Pro Glu Ile Cys	
133	50 55 60	
136	Pro Gln Ser Lys Ala Gln Arg Cys Gln Pro Asn Glu His Asn Cys Leu	
137	65 70 75 80	
140	Gly Thr Glu Leu Cys Val Pro Met Ser Arg Leu Cys Asn Gly Val Gln	
141	85 90 95	
144	Asp Cys Met Asp Gly Ser Asp Glu Gly Pro His Cys Arg Glu Leu Gln	
145	100 105 110	
148	Gly Asn Cys Ser Arg Leu Gly Cys Gln His His Cys Val Pro Thr Leu	
149	115 120 125	
152	Asp Gly Pro Thr Cys Tyr Cys Asn Ser Ser Phe Gln Leu Gln Ala Asp	
153	130 135 140	
156	Gly Lys Thr Cys Lys Asp Phe Asp Glu Cys Ser Val Tyr Gly Thr Cys	
157	145 150 155 160	
160	Ser Gln Leu Cys Thr Asn Thr Asp Gly Ser Phe Ile Cys Gly Cys Val	
161	165 170 175	
164	Glu Gly Tyr Leu Leu Gln Pro Asp Asn Arg Ser Cys Lys Ala Lys Asn	
165	180 185 190	
168	Glu Pro Val Asp Arg Pro Pro Val Leu Leu Ile Ala Asn Ser Gln Asn	
169	195 200 205	
172	Ile Leu Ala Thr Tyr Leu Ser Gly Ala Gln Val Ser Thr Ile Thr Pro	

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**Output Set: N:\CRF4\04132005\J530393.raw**

173	210	215	220	
176	Thr Ser Thr Arg Gln Thr Thr Ala Met Asp Phe Ser Tyr Ala Asn Glu			
177	225	230	235	240
180	Thr Val Cys Trp Val His Val Gly Asp Ser Ala Ala Gln Thr Gln Leu			
181	245	250	255	
184	Lys Cys Ala Arg Met Pro Gly Leu Lys Gly Phe Val Asp Glu His Thr			
185	260	265	270	
188	Ile Asn Ile Ser Leu Ser Leu His His Val Glu Gln Met Ala Ile Asp			
189	275	280	285	
192	Trp Leu Thr Gly Asn Phe Tyr Phe Val Asp Asp Ile Asp Asp Arg Ile			
193	290	295	300	
196	Phe Val Cys Asn Arg Asn Gly Asp Thr Cys Val Thr Leu Leu Asp Leu			
197	305	310	315	320
200	Glu Leu Tyr Asn Pro Lys Gly Ile Ala Leu Asp Pro Ala Met Gly Lys			
201	325	330	335	
204	Val Phe Phe Thr Asp Tyr Gly Gln Ile Pro Lys Val Glu Arg Cys Asp			
205	340	345	350	
208	Met Asp Gly Gln Asn Arg Thr Lys Leu Val Asp Ser Lys Ile Val Phe			
209	355	360	365	
212	Pro His Gly Ile Thr Leu Asp Leu Val Ser Arg Leu Val Tyr Trp Ala			
213	370	375	380	
216	Asp Ala Tyr Leu Asp Tyr Ile Glu Val Val Asp Tyr Glu Gly Lys Gly			
217	385	390	395	400
220	Arg Gln Thr Ile Ile Gln Gly Ile Leu Ile Glu His Leu Tyr Gly Leu			
221	405	410	415	
224	Thr Val Phe Glu Asn Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Ala Asn			
225	420	425	430	
228	Ala Gln Gln Lys Thr Ser Val Ile Arg Val Asn Arg Phe Asn Ser Thr			
229	435	440	445	
232	Glu Tyr Gln Val Val Thr Arg Val Asp Lys Gly Gly Ala Leu His Ile			
233	450	455	460	
236	Tyr His Gln Arg Arg Gln Pro Arg Val Arg Ser His Ala Cys Glu Asn			
237	465	470	475	480
240	Asp Gln Tyr Gly Lys Pro Gly Gly Cys Ser Asp Ile Cys Leu Leu Ala			
241	485	490	495	
244	Asn Ser His Lys Ala Arg Thr Cys Arg Cys Arg Ser Gly Phe Ser Leu			
245	500	505	510	
248	Gly Ser Asp Gly Lys Ser Cys Lys Lys Pro Glu His Glu Leu Phe Leu			
249	515	520	525	
252	Val Tyr Gly Lys Gly Arg Pro Gly Ile Ile Arg Gly Met Asp Met Gly			
253	530	535	540	
256	Ala Lys Val Pro Asp Glu His Met Ile Pro Ile Glu Asn Leu Met Asn			
257	545	550	555	560
260	Pro Arg Ala Leu Asp Phe His Ala Glu Thr Gly Phe Ile Tyr Phe Ala			
261	565	570	575	
264	Asp Thr Thr Ser Tyr Leu Ile Gly Arg Gln Lys Ile Asp Gly Thr Glu			
265	580	585	590	
268	Arg Glu Thr Ile Leu Lys Asp Gly Ile His Asn Val Glu Gly Val Ala			
269	595	600	605	

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272 Val Asp Trp Met Gly Asp Asn Leu Tyr Trp Thr Asp Asp Gly Pro Lys  
 273 610 615 620  
 276 Lys Thr Ile Ser Val Ala Arg Leu Glu Lys Ala Ala Gln Thr Arg Lys  
 277 625 630 635 640  
 280 Thr Leu Ile Glu Gly Lys Met Thr His Pro Arg Ala Ile Met Val Asp  
 281 645 650 655  
 284 Pro Leu Asn Gly Trp Met Tyr Trp Thr Asp Trp Glu Glu Asp Pro Lys  
 285 660 665 670  
 288 Asp Ser Arg Arg Gly Arg Leu Glu Arg Ala Trp Met Asp Gly Ser His  
 289 675 680 685  
 292 Arg Asp Ile Phe Val Thr Ser Lys Thr Val Leu Trp Pro Asn Gly Leu  
 293 690 695 700  
 296 Ser Leu Asp Ile Pro Ala Gly Arg Leu Tyr Trp Val Asp Ala Phe Tyr  
 297 705 710 715 720  
 300 Asp Arg Ile Glu Thr Ile Leu Leu Asn Gly Thr Asp Arg Lys Ile Val  
 301 725 730 735  
 304 Tyr Glu Gly Pro Glu Leu Asn His Ala Phe Gly Leu Cys His His Gly  
 305 740 745 750  
 308 Asn Tyr Leu Phe Trp Thr Glu Tyr Arg Ser Gly Ser Val Tyr Arg Leu  
 309 755 760 765  
 312 Glu Arg Gly Val Gly Gly Ala Pro Pro Thr Val Thr Leu Leu Arg Ser  
 313 770 775 780  
 316 Glu Arg Pro Pro Ile Phe Glu Ile Arg Met Tyr Asp Ala Gln Gln Gln  
 317 785 790 795 800  
 320 Gln Val Gly Thr Asn Lys Cys Arg Val Asn Asn Gly Gly Cys Ser Ser  
 321 805 810 815  
 324 Leu Cys Leu Ala Thr Pro Gly Ser Arg Gln Cys Ala Cys Ala Glu Asp  
 325 820 825 830  
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 329 835 840 845  
 332 Val Pro Pro  
 333 850  
 336 <210> SEQ ID NO: 3  
 337 <211> LENGTH: 896  
 338 <212> TYPE: PRT  
 339 <213> ORGANISM: H. sapiens  
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 343 Met Leu Thr Pro Pro Leu Leu Leu Leu Pro Leu Leu Ser Ala Leu  
 344 1 5 10 15  
 347 Ala Ala Ala Ala Ile Asp Ala Pro Lys Thr Cys Ser Pro Lys Gln Phe  
 348 20 25 30  
 351 Ala Cys Arg Asp Gln Ile Thr Cys Ile Ser Lys Gly Trp Arg Cys Asp  
 352 35 40 45  
 355 Gly Glu Arg Asp Cys Pro Asp Gly Ser Asp Glu Ala Pro Glu Ile Cys  
 356 50 55 60  
 359 Pro Gln Ser Lys Ala Gln Arg Cys Gln Pro Asn Glu His Asn Cys Leu  
 360 65 70 75 80  
 363 Gly Thr Glu Leu Cys Val Pro Met Ser Arg Leu Cys Asn Gly Val Gln  
 364 85 90 95

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367 Asp Cys Met Asp Gly Ser Asp Glu Gly Pro His Cys Arg Glu Leu Gln  
 368 100 105 110  
 371 Gly Asn Cys Ser Arg Leu Gly Cys Gln His His Cys Val Pro Thr Leu  
 372 115 120 125  
 375 Asp Gly Pro Thr Cys Tyr Cys Asn Ser Ser Phe Gln Leu Gln Ala Asp  
 376 130 135 140  
 379 Gly Lys Thr Cys Lys Asp Phe Asp Glu Cys Ser Val Tyr Gly Thr Cys  
 380 145 150 155 160  
 383 Ser Gln Leu Cys Thr Asn Thr Asp Gly Ser Phe Ile Cys Gly Cys Val  
 384 165 170 175  
 387 Glu Gly Tyr Leu Leu Gln Pro Asp Asn Arg Ser Cys Lys Ala Lys Asn  
 388 180 185 190  
 391 Glu Pro Val Asp Arg Pro Pro Val Leu Leu Ile Ala Asn Ser Gln Asn  
 392 195 200 205  
 395 Ile Leu Ala Thr Tyr Leu Ser Gly Ala Gln Val Ser Thr Ile Thr Pro  
 396 210 215 220  
 399 Thr Ser Thr Arg Gln Thr Thr Ala Met Asp Phe Ser Tyr Ala Asn Glu  
 400 225 230 235 240  
 403 Thr Val Cys Trp Val His Val Gly Asp Ser Ala Ala Gln Thr Gln Leu  
 404 245 250 255  
 407 Lys Cys Ala Arg Met Pro Gly Leu Lys Gly Phe Val Asp Glu His Thr  
 408 260 265 270  
 411 Ile Asn Ile Ser Leu Ser Leu His His Val Glu Gln Met Ala Ile Asp  
 412 275 280 285  
 415 Trp Leu Thr Gly Asn Phe Tyr Phe Val Asp Asp Ile Asp Asp Arg Ile  
 416 290 295 300  
 419 Phe Val Cys Asn Arg Asn Gly Asp Thr Cys Val Thr Leu Leu Asp Leu  
 420 305 310 315 320  
 423 Glu Leu Tyr Asn Pro Lys Gly Ile Ala Leu Asp Pro Ala Met Gly Lys  
 424 325 330 335  
 427 Val Phe Phe Thr Asp Tyr Gly Gln Ile Pro Lys Val Glu Arg Cys Asp  
 428 340 345 350  
 431 Met Asp Gly Gln Asn Arg Thr Lys Leu Val Asp Ser Lys Ile Val Phe  
 432 355 360 365  
 435 Pro His Gly Ile Thr Leu Asp Leu Val Ser Arg Leu Val Tyr Trp Ala  
 436 370 375 380  
 439 Asp Ala Tyr Leu Asp Tyr Ile Glu Val Val Asp Tyr Glu Gly Lys Gly  
 440 385 390 395 400  
 443 Arg Gln Thr Ile Ile Gln Gly Ile Leu Ile Glu His Leu Tyr Gly Leu  
 444 405 410 415  
 447 Thr Val Phe Glu Asn Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Ala Asn  
 448 420 425 430  
 451 Ala Gln Gln Lys Thr Ser Val Ile Arg Val Asn Arg Phe Asn Ser Thr  
 452 435 440 445  
 455 Glu Tyr Gln Val Val Thr Arg Val Asp Lys Gly Gly Ala Leu His Ile  
 456 450 455 460  
 459 Tyr His Gln Arg Arg Gln Pro Arg Val Arg Ser His Ala Cys Glu Asn  
 460 465 470 475 480  
 463 Asp Gln Tyr Gly Lys Pro Gly Gly Cys Ser Asp Ile Cys Leu Leu Ala

**VERIFICATION SUMMARY**  
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Input Set : D:\8449304999.txt  
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date